

## SEQUENCE LISTING

<110> FEDER, J. N.

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<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY5,  
EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES

<130> D0041NP/3053-4118US3

<140> TBA

<141> 2001-09-26

<150> 60/235,713

<151> 2000-09-27

<150> 60/261,781

<151> 2001-01-16

<150> 60/306,605

<151> 2001-07-19

<150> 60/310,436

<151> 2001-08-03

<160> 61

<170> PatentIn Ver. 2.1

<210> 1

<211> 2214

<212> DNA

<213> Homo sapiens

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tgcttacccc gagctttca ctgtgatggc aaggatgact gtggaaacgg ggccggacgaa 180  
gagaactgtg gtgacactag tggatggcg accatatttgc acagactgca tggaaatgtct 240  
aacagcgtgg ccttaacaca ggagtgcctt ctaaaacagt atccacaatgc ctgtgactgc 300  
aaagaaactcg aatttggatgt tgtaaatgtt gactttaaagt ctgtgcggat gatttctaaac 360  
aatgtgacat tactgtctt taagaaaacca aaaaatccaca gtctccaga taaaatttc 420  
atcaaataca caaaatcaa aaagatattt cttcagcata attcgatttgc acacatatcc 480  
aggaaagcat tttttggatt atgtaatgtt caaatattt atctcaacca caactgcattc 540  
acaaccctca gacctggaat attcaagac ttacatcgc taacttggtt aattcttagat 600  
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103260-9255860

<210> 2

<211> 737

<212> PRT

<213> *Homo sapiens*

<400> 2

Met Phe Phe Leu Leu His Phe Ile Val Leu Ile Asn Val Lys Asp Phe

1

6

14

15

Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr  
 20 25 30

Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys  
35 40 45

Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly  
 50 55 60

Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala  
65 70 75 80

Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln	85	90	95	
Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu	100	105	110	
Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys	115	120	125	
Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr	130	135	140	
Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser	145	150	155	160
Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu Asn	165	170	175	
His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu His	180	185	190	
Gln Leu Thr Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile Ser	195	200	205	
Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met Val	210	215	220	
Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met Pro	225	230	235	240
Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu Thr	245	250	255	
Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Phe Leu Pro	260	265	270	
Arg Asn Gln Ile Gly Phe Val Pro Glu Lys Thr Phe Ser Ser Leu Lys	275	280	285	
Asn Leu Gly Glu Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser	290	295	300	
Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asn Leu Ser	305	310	315	320
Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln Phe Glu Ser Leu Lys	325	330	335	

Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile Asn  
340 345 350

Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe Lys  
355 360 365

Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val Arg Ile Cys Met Pro  
370 375 380

Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn Ile  
385 390 395 400

Leu Arg Ile Phe Val Trp Val Ile Ala Phe Ile Thr Cys Phe Gly Asn  
405 410 415

Leu Phe Val Ile Gly Met Arg Ser Phe Ile Lys Ala Glu Asn Thr Thr  
420 425 430

His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala Asp Cys Leu Met Gly  
435 440 445

Val Tyr Leu Phe Phe Val Gly Ile Phe Asp Ile Lys Tyr Arg Gly Gln  
450 455 460

Tyr Gln Lys Tyr Ala Leu Leu Trp Met Glu Ser Val Gln Cys Arg Leu  
465 470 475 480

Met Gly Phe Leu Ala Met Leu Ser Thr Glu Val Ser Val Leu Leu Leu  
485 490 495

Thr Tyr Leu Thr Leu Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser  
500 505 510

Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile Cys Ile  
515 520 525

Trp Met Ala Gly Phe Leu Ile Ala Val Ile Pro Phe Trp Asn Lys Asp  
530 535 540

Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu Tyr  
545 550 555 560

Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser Leu Gly Ile  
565 570 575

Phe Leu Gly Val Asn Leu Leu Ala Phe Leu Ile Ile Val Phe Ser Tyr  
580 585 590

Ile Thr Met Phe Cys Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr Glu  
595 600 605

Val Arg Asn Cys Phe Gly Arg Glu Val Ala Val Ala Asn Arg Phe Phe  
610 615 620

Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val Val  
625 630 635 640

Lys Ile Leu Ser Leu Phe Arg Val Glu Ile Pro Asp Thr Met Thr Ser  
645 650 655

Trp Ile Val Ile Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro Ile  
660 665 670

Leu Tyr Thr Leu Thr Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln Leu  
675 680 685

Leu His Lys His Gln Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys Ser  
690 695 700

Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser Ser Ser Leu Lys Leu  
705 710 715 720

Gly Val Leu Asn Lys Ile Thr Leu Gly Asp Ser Ile Met Lys Pro Val  
725 730 735

Ser

<210> 3

<211> 17

<212> DNA

<213> Homo sapiens

<400> 3

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17

<210> 4

<211> 1026

<212> DNA

<213> Homo sapiens

<400> 4

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<212> DNA  
<213> *Homo sapiens*

<210> 6

<211> 713

<212> PRT

<213> *Homo sapiens*

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Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly Tyr  
 20 25 30

Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His Cys  
 35 40 45

Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys Gly  
50 55 60

Asp	Thr	Ser	Gly	Trp	Ala	Thr	Ile	Phe	Gly	Thr	Val	His	Gly	Asn	Ala
65					70					75					80

Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro Gln	85	90	95
---	----	----	----

Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp Leu  
                  100                 105                 110

Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys  
115 120 125

Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr Thr  
 130 135 140

Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile Ser  
 145 150 155 160

Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Ile Leu Asp  
 165 170 175

Asp Asn Pro Ile Thr Arg Ile Ser Gln Arg Leu Phe Thr Gly Leu Asn  
 180 185 190

Ser Leu Phe Phe Leu Ser Met Val Asn Asn Tyr Leu Glu Ala Leu Pro  
 195 200 205

Lys Gln Met Cys Ala Gln Met Pro Gln Leu Asn Trp Val Asp Leu Glu  
 210 215 220

Gly Asn Arg Ile Lys Tyr Leu Thr Asn Ser Thr Phe Leu Ser Cys Asp  
 225 230 235 240

Ser Leu Thr Val Leu Phe Leu Pro Arg Asn Gln Ile Gly Phe Val Pro  
 245 250 255

Glu Lys Thr Phe Ser Ser Leu Lys Asn Leu Gly Glu Leu Asp Leu Ser  
 260 265 270

Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu Phe Lys Asp Leu Lys  
 275 280 285

Leu Leu Gln Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr Leu His  
 290 295 300

Lys Asn Gln Phe Glu Ser Leu Lys Gln Leu Gln Ser Leu Asp Leu Glu  
 305 310 315 320

Arg Ile Glu Ile Pro Asn Ile Asn Thr Arg Met Phe Gln Pro Met Lys  
 325 330 335

Asn Leu Ser His Ile Tyr Phe Lys Asn Phe Arg Tyr Cys Ser Tyr Ala  
 340 345 350

Pro His Val Arg Ile Cys Met Pro Leu Thr Asp Gly Ile Ser Ser Phe  
 355 360 365

Glu Asp Leu Leu Ala Asn Asn Ile Leu Arg Ile Phe Val Trp Val Ile  
 370 375 380

Ala Phe Ile Thr Cys Phe Gly Asn Leu Phe Val Ile Gly Met Arg Ser  
 385 390 395 400



Phe Lys Asp Lys Leu Lys Gln Leu Leu His His Gln Arg Lys Ser  
660 665 670

Ile Phe Lys Ile Lys Lys Ser Leu Ser Thr Ser Ile Val Trp Ile  
675 680 685

Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu Asn Lys Ile Thr Leu  
690 695 700

Gly Asp Ser Ile Met Lys Pro Val Ser  
705 710

<210> 7

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY4 5'  
primer

<400> 7

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tgccgttttc caggtcgaat 80

<210> 8

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
oligos

<400> 8

aagcagatgt gtgcccaaat g 21

<210> 9

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
oligos

09065536 - 092501

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24

<210> 10  
<211> 1115  
<212> PRT  
<213> Lymnaea stagnalis

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Ser Pro Pro Thr Leu Cys Ser Val Glu Gly Thr Phe His Cys Asp Asp  
35 40 45  
Gly Met Leu Gln Cys Val Leu Met Gly Ser Lys Cys Asp Gly Val Ser  
50 55 60  
Asp Cys Glu Asn Gly Met Asp Glu Ser Val Glu Thr Cys Gly Cys Leu  
65 70 75 80  
Gln Ser Glu Phe Gln Cys Asn His Thr Thr Cys Ile Asp Lys Ile Leu  
85 90 95  
Arg Cys Asp Arg Asn Asp Asp Cys Ser Asn Gly Leu Asp Glu Arg Glu  
100 105 110  
Cys Asp Ile Tyr Ile Cys Pro Leu Gly Thr His Val Lys Trp His Asn  
115 120 125  
His Phe Cys Val Pro Arg Asp Lys Gln Cys Asp Phe Leu Asp Asp Cys  
130 135 140  
Gly Asp Asn Ser Asp Glu Lys Ile Cys Glu Arg Arg Glu Cys Val Ala  
145 150 155 160  
Thr Glu Phe Lys Cys Asn Asn Ser Gln Cys Val Ala Phe Gly Asn Leu  
165 170 175  
Cys Asp Gly Leu Val Asp Cys Val Asp Gly Ser Asp Glu Asp Gln Val  
180 185 190  
Ala Cys Asp Ser Asp Lys Tyr Phe Gln Cys Ala Glu Gly Ser Leu Ile

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195 200 205  
Lys Lys Glu Phe Val Cys Asp Gly Trp Val Asp Cys Lys Leu Thr Phe  
210 215 220  
Ala Asp Glu Leu Asn Cys Lys Leu Cys Asp Glu Asp Asp Phe Arg Cys  
225 230 235 240  
Ser Asp Thr Arg Cys Ile Gln Lys Ser Asn Val Cys Asp Gly Tyr Cys  
245 250 255  
Asp Cys Lys Thr Cys Asp Asp Glu Val Cys Ala Asn Asn Thr Tyr  
260 265 270  
Gly Cys Pro Met Asp Thr Lys Tyr Met Cys Arg Ser Ile Tyr Gly Glu  
275 280 285  
Pro Arg Cys Ile Asp Lys Asp Asn Val Cys Asn Met Ile Asn Asp Cys  
290 295 300  
Arg Asp Gly Asn Val Gly Thr Asp Glu Tyr Tyr Cys Ser Asn Asp Ser  
305 310 315 320  
Glu Cys Lys Asn Phe Gln Ala Ala Met Gly Phe Phe Tyr Cys Pro Glu  
325 330 335  
Glu Arg Cys Leu Ala Lys His Leu Tyr Cys Asp Leu His Pro Asp Cys  
340 345 350  
Ile Asn Gly Glu Asp Glu Gln Ser Cys Leu Ala Pro Pro Lys Cys Ser  
355 360 365  
Gln Asp Glu Phe Gln Cys His His Gly Lys Cys Ile Pro Ile Ser Lys  
370 375 380  
Arg Cys Asp Ser Val His Asp Cys Val Asp Trp Ser Asp Glu Met Asn  
385 390 395 400  
Cys Glu Asn His Gln Cys Ala Ala Asn Met Lys Ser Cys Leu Ser Gly  
405 410 415  
His Cys Ile Glu Glu His Lys Trp Cys Asn Phe His Arg Glu Cys Pro  
420 425 430  
Asp Gly Ser Asp Glu Lys Asp Cys Asp Pro Arg Pro Val Cys Glu Ala  
435 440 445  
Asn Gln Phe Arg Cys Lys Asn Gly Gln Cys Ile Asp Pro Leu Gln Val

450	455	460
Cys Val Lys Gly Asp Lys Tyr Asp Gly Cys Ala Asp Gln Ser His Leu		
465	470	475
		480
Ile Asn Cys Ser Gln His Ile Cys Leu Glu Gly Gln Phe Arg Cys Arg		
	485	490
		495
Lys Ser Phe Cys Ile Asn Gln Thr Lys Val Cys Asp Gly Thr Val Asp		
	500	505
		510
Cys Leu Gln Gly Met Trp Asp Glu Asn Asn Cys Arg Tyr Trp Cys Pro		
	515	520
		525
His Gly Gln Ala Ile Cys Gln Cys Glu Gly Val Thr Met Asp Cys Thr		
	530	535
		540
Gly Gln Lys Leu Lys Glu Met Pro Val Gln Gln Met Glu Glu Asp Leu		
	545	550
		555
		560
Ser Lys Leu Met Ile Gly Asp Asn Leu Leu Asn Leu Thr Ser Thr Thr		
	565	570
		575
Phe Ser Ala Thr Tyr Tyr Asp Lys Val Thr Tyr Leu Asp Leu Ser Arg		
	580	585
		590
Asn His Leu Thr Glu Ile Pro Ile Tyr Ser Phe Gln Asn Met Trp Lys		
	595	600
		605
Leu Thr His Leu Asn Leu Ala Asp Asn Asn Ile Thr Ser Leu Lys Asn		
	610	615
		620
Gly Ser Leu Leu Gly Leu Ser Asn Leu Lys Gln Leu His Ile Asn Gly		
	625	630
		635
		640
Asn Lys Ile Glu Thr Ile Glu Glu Asp Thr Phe Ser Ser Met Ile His		
	645	650
		655
Leu Thr Val Leu Asp Leu Ser Asn Gln Arg Leu Thr His Val Tyr Lys		
	660	665
		670
Asn Met Phe Lys Gly Leu Lys Gln Ile Thr Val Leu Asn Ile Ser Arg		
	675	680
		685
Asn Gln Ile Asn Ser Ile Asp Asn Gly Ala Phe Asn Asn Leu Ala Asn		
	690	695
		700
Val Arg Leu Ile Asp Leu Ser Gly Asn Val Ile Lys Asp Ile Gly Gln		

TOS260-36559660

705	710	715	720
Lys Val Phe Met Gly Leu Pro Arg Leu Val Glu Leu Lys Thr Asp Ser			
725	730	735	
Tyr Arg Phe Cys Cys Leu Ala Pro Glu Gly Val Lys Cys Ser Pro Lys			
740	745	750	
Gln Asp Glu Phe Ser Ser Cys Glu Asp Leu Met Ser Asn His Val Leu			
755	760	765	
Arg Val Ser Ile Trp Val Leu Gly Val Ile Ala Leu Val Gly Asn Phe			
770	775	780	
Val Val Ile Phe Trp Arg Val Arg Asp Phe Arg Gly Gly Lys Val His			
785	790	795	800
Ser Phe Leu Ile Thr Asn Leu Ala Ile Gly Asp Phe Leu Met Gly Val			
805	810	815	
Tyr Leu Leu Ile Ile Ala Thr Ala Asp Thr Tyr Tyr Arg Gly Val Tyr			
820	825	830	
Ile Ser His Asp Glu Asn Trp Lys Gln Ser Gly Leu Cys Gln Phe Ala			
835	840	845	
Gly Phe Val Ser Thr Phe Ser Ser Glu Leu Ser Val Leu Thr Leu Ser			
850	855	860	
Thr Ile Thr Leu Asp Arg Leu Ile Cys Ile Leu Phe Pro Leu Arg Arg			
865	870	875	880
Thr Arg Leu Gly Leu Arg Gln Ala Ile Ile Val Met Ser Cys Ile Trp			
885	890	895	
Val Leu Val Phe Leu Leu Ala Val Leu Pro Leu Leu Gly Phe Ser Tyr			
900	905	910	
Phe Glu Asn Phe Tyr Gly Arg Ser Gly Val Cys Leu Ala Leu His Val			
915	920	925	
Thr Pro Asp Arg Arg Pro Gly Trp Glu Tyr Ser Val Gly Val Phe Ile			
930	935	940	
Leu Leu Asn Leu Leu Ser Phe Val Leu Ile Ala Ser Ser Tyr Leu Trp			
945	950	955	960
Met Phe Ser Val Ala Lys Lys Thr Arg Ser Ala Val Arg Thr Ala Glu			

108260-98559660

965

970

975

Ser Lys Asn Asp Asn Ala Met Ala Arg Arg Met Thr Leu Ile Val Met  
980 985 990

Thr Asp Phe Cys Cys Trp Val Pro Ile Ile Val Leu Gly Phe Val Ser  
995 1000 1005

Leu Ala Gly Ala Arg Ala Asp Asp Gln Val Tyr Ala Trp Ile Ala Val  
1010 1015 1020

Phe Val Leu Pro Leu Asn Ser Ala Thr Asn Pro Val Ile Tyr Thr Leu  
1025 1030 1035 1040

Ser Thr Ala Pro Phe Leu Gly Asn Val Arg Lys Arg Ala Asn Arg Phe  
1045 1050 1055

Arg Lys Ser Phe Ile His Ser Phe Thr Gly Asp Thr Lys His Ser Tyr  
1060 1065 1070

Val Asp Asp Gly Thr Thr His Ser Tyr Cys Glu Lys Lys Ser Pro Tyr  
1075 1080 1085

Arg Gln Leu Glu Leu Lys Arg Leu Arg Ser Leu Asn Ser Ser Pro Pro  
1090 1095 1100

Met Tyr Tyr Asn Thr Glu Leu His Ser Asp Ser  
1105 1110 1115

<210> 11

<211> 692

<212> PRT

<213> RAT

<400> 11

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Gly Cys His His Trp Leu Cys His Cys Ser Asn Arg Val Phe Leu Cys  
20 25 30

Gln Asp Ser Lys Val Thr Glu Ile Pro Thr Asp Leu Pro Arg Asn Ala  
35 40 45

Ile Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Pro Lys Gly  
50 55 60

Ser Phe Ala Gly Phe Gly Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn  
 65 70 75 80

Asp Val Leu Glu Val Ile Glu Ala Asp Val Phe Ser Asn Leu Pro Lys  
 85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asn  
 100 105 110

Pro Glu Ala Phe Gln Asn Leu Pro Ser Leu Arg Tyr Leu Leu Ile Ser  
 115 120 125

Asn Thr Gly Ile Lys His Leu Pro Ala Val His Lys Ile Gln Ser Leu  
 130 135 140

Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Ile Val  
 145 150 155 160

Ala Arg Asn Ser Phe Met Gly Leu Ser Phe Glu Ser Val Ile Leu Trp  
 165 170 175

Leu Ser Lys Asn Gly Ile Glu Glu Ile His Asn Cys Ala Phe Asn Gly  
 180 185 190

Thr Gln Leu Asp Glu Leu Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu  
 195 200 205

Leu Pro Asn Asp Val Phe Gln Gly Ala Ser Gly Pro Val Ile Leu Asp  
 210 215 220

Ile Ser Arg Thr Lys Val His Ser Leu Pro Asn His Gly Leu Glu Asn  
 225 230 235 240

Leu Lys Lys Leu Arg Ala Arg Ser Thr Tyr Arg Leu Lys Lys Leu Pro  
 245 250 255

Asn Leu Asp Lys Phe Val Thr Leu Met Glu Ala Ser Leu Thr Tyr Pro  
 260 265 270

Ser His Cys Cys Ala Phe Ala Asn Leu Lys Arg Gln Ile Ser Glu Leu  
 275 280 285

His Pro Ile Cys Asn Lys Ser Ile Leu Arg Gln Asp Ile Asp Asp Met  
 290 295 300

Thr Gln Ile Gly Asp Gln Arg Val Ser Leu Ile Asp Asp Glu Pro Ser  
 305 310 315 320

Tyr Gly Lys Gly Ser Asp Met Met Tyr Asn Glu Phe Asp Tyr Asp Leu  
 325 330 335  
  
 Cys Asn Glu Val Val Asp Val Thr Cys Ser Pro Lys Pro Asp Ala Phe  
 340 345 350  
  
 Asn Pro Cys Glu Asp Ile Met Gly Tyr Asn Ile Leu Arg Val Leu Ile  
 355 360 365  
  
 Trp Phe Ile Ser Ile Leu Ala Ile Thr Gly Asn Thr Thr Val Leu Val  
 370 375 380  
  
 Val Leu Thr Thr Ser Gln Tyr Lys Leu Thr Val Pro Arg Phe Leu Met  
 385 390 395 400  
  
 Cys Asn Leu Ala Phe Ala Asp Leu Cys Ile Gly Ile Tyr Leu Leu  
 405 410 415  
  
 Ile Ala Ser Val Asp Ile His Thr Lys Ser Gln Tyr His Asn Tyr Ala  
 420 425 430  
  
 Ile Asp Trp Gln Thr Gly Ala Gly Cys Asp Ala Ala Gly Phe Phe Thr  
 435 440 445  
  
 Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu Thr Ala Ile Thr Leu  
 450 455 460  
  
 Glu Arg Trp His Thr Ile Thr His Ala Met Gln Leu Glu Cys Lys Val  
 465 470 475 480  
  
 Gln Leu Arg His Ala Ala Ser Val Met Val Leu Gly Trp Thr Phe Ala  
 485 490 495  
  
 Phe Ala Ala Ala Leu Phe Pro Ile Phe Gly Ile Ser Ser Tyr Met Lys  
 500 505 510  
  
 Val Ser Ile Cys Leu Pro Met Asp Ile Asp Ser Pro Leu Ser Gln Leu  
 515 520 525  
  
 Tyr Val Met Ala Leu Leu Val Leu Asn Val Leu Ala Phe Val Val Ile  
 530 535 540  
  
 Cys Gly Cys Tyr Thr His Ile Tyr Leu Thr Val Arg Asn Pro Thr Ile  
 545 550 555 560  
  
 Val Ser Ser Ser Ser Asp Thr Lys Ile Ala Lys Arg Met Ala Thr Leu  
 565 570 575

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Ile Phe Thr Asp Phe Leu Cys Met Ala Pro Ile Ser Phe Phe Ala Ile  
 580 585 590

Ser Ala Ser Leu Lys Val Pro Leu Ile Thr Val Ser Lys Ala Lys Ile  
 595 600 605

Leu Leu Val Leu Phe Tyr Pro Ile Asn Ser Cys Ala Asn Pro Phe Leu  
 610 615 620

Tyr Ala Ile Phe Thr Lys Asn Phe Arg Arg Asp Phe Phe Ile Leu Leu  
 625 630 635 640

Ser Lys Phe Gly Cys Tyr Glu Met Gln Ala Gln Ile Tyr Arg Thr Glu  
 645 650 655

Thr Ser Ser Ala Thr His Asn Phe His Ala Arg Lys Ser His Cys Ser  
 660 665 670

Ser Ala Pro Arg Val Thr Asn Ser Tyr Val Leu Val Pro Leu Asn His  
 675 680 685

Ser Ser Gln Asn  
 690

<210> 12  
 <211> 688  
 <212> PRT  
 <213> Rattus norvegicus

<400> 12  
 Met Ala Leu Leu Leu Val Ser Leu Leu Ala Phe Leu Gly Thr Gly Ser  
 1 5 10 15

Gly Cys His His Trp Leu Cys His Cys Ser Asn Arg Val Phe Leu Cys  
 20 25 30

Gln Asp Ser Lys Val Thr Glu Ile Pro Thr Asp Leu Pro Arg Asn Ala  
 35 40 45

Ile Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Pro Lys Gly  
 50 55 60

Ser Phe Ala Gly Phe Gly Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn  
 65 70 75 80

Asp Val Leu Glu Val Ile Glu Ala Asp Val Phe Ser Asn Leu Pro Lys  
 85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asn  
 100 105 110  
  
 Pro Glu Ala Phe Gln Asn Leu Pro Ser Leu Arg Tyr Leu Leu Ile Ser  
 115 120 125  
  
 Asn Thr Gly Ile Lys His Leu Pro Ala Val His Lys Ile Gln Ser Leu  
 130 135 140  
  
 Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Ile Val  
 145 150 155 160  
  
 Ala Arg Asn Ser Phe Met Gly Leu Ser Phe Glu Trp Leu Ser Lys Asn  
 165 170 175  
  
 Gly Ile Glu Glu Ile His Asn Cys Ala Phe Asn Gly Thr Gln Leu Asp  
 180 185 190  
  
 Glu Leu Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu Leu Pro Asn Asp  
 195 200 205  
  
 Val Phe Gln Gly Ala Ser Gly Pro Val Ile Leu Asp Ile Ser Arg Thr  
 210 215 220  
  
 Lys Val His Ser Leu Pro Asn His Gly Leu Glu Asn Leu Lys Lys Leu  
 225 230 235 240  
  
 Arg Ala Arg Ser Thr Tyr Arg Trp Lys Lys Leu Pro Asn Leu Asp Lys  
 245 250 255  
  
 Phe Val Thr Leu Met Glu Ala Ser Leu Thr Tyr Pro Ser His Cys Cys  
 260 265 270  
  
 Ala Phe Ala Asn Leu Lys Arg Gln Ile Ser Glu Leu His Pro Ile Cys  
 275 280 285  
  
 Asn Lys Ser Ile Leu Arg Gln Asp Ile Asp Asp Met Thr Gln Ile Gly  
 290 295 300  
  
 Asp Gln Arg Val Ser Leu Ile Asp Asp Glu Pro Ser Tyr Gly Lys Gly  
 305 310 315 320  
  
 Ser Asp Met Met Tyr Asn Glu Phe Asp Tyr Asp Leu Cys Asn Glu Val  
 325 330 335  
  
 Val Asp Val Thr Cys Ser Pro Lys Pro Asp Ala Phe Asn Pro Cys Glu  
 340 345 350

Asp Ile Met Gly Tyr Asn Ile Leu Arg Val Leu Ile Trp Phe Ile Ser			
355	360	365	
Ile Leu Ala Ile Thr Gly Asn Thr Thr Val Leu Val Val Leu Thr Thr			
370	375	380	
Ser Gln Tyr Lys Leu Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ala			
385	390	395	400
Phe Ala Asp Leu Cys Ile Gly Ile Tyr Leu Leu Leu Ile Ala Ser Val			
405	410	415	
Asp Ile His Thr Lys Ser Gln Tyr His Asn Tyr Ala Ile Asp Trp Gln			
420	425	430	
Thr Gly Ala Gly Cys Asp Ala Ala Gly Phe Phe Thr Val Phe Ala Ser			
435	440	445	
Glu Leu Ser Val Tyr Thr Leu Thr Ala Ile Thr Leu Glu Arg Trp His			
450	455	460	
Thr Ile Thr His Ala Met Gln Leu Glu Cys Lys Val Gln Leu Arg His			
465	470	475	480
Ala Ala Ser Val Met Val Leu Gly Trp Thr Phe Ala Phe Ala Ala Ala			
485	490	495	
Leu Phe Pro Ile Phe Gly Ile Ser Ser Tyr Met Lys Val Ser Ile Cys			
500	505	510	
Leu Pro Met Asp Ile Asp Ser Pro Leu Ser Gln Leu Tyr Val Met Ala			
515	520	525	
Leu Leu Val Leu Asn Val Leu Ala Phe Val Val Ile Cys Gly Cys Tyr			
530	535	540	
Thr His Ile Tyr Leu Thr Val Arg Asn Pro Thr Ile Val Ser Ser Ser			
545	550	555	560
Ser Asp Thr Lys Ile Ala Lys Arg Met Ala Thr Leu Ile Phe Thr Asp			
565	570	575	
Phe Leu Cys Met Ala Pro Ile Ser Phe Phe Ala Ile Ser Ala Ser Leu			
580	585	590	
Lys Val Pro Leu Ile Thr Val Ser Lys Ala Lys Ile Leu Leu Val Leu			
595	600	605	

Phe Tyr Pro Ile Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe  
 610 615 620  
  
 Thr Lys Asn Phe Arg Arg Asp Phe Phe Ile Leu Leu Ser Lys Phe Gly  
 625 630 635 640  
  
 Cys Tyr Glu Met Gln Ala Gln Ile Tyr Arg Thr Glu Thr Ser Ser Ala  
 645 650 655  
  
 Thr His Asn Phe His Ala Arg Lys Ser His Cys Ser Ser Ala Pro Arg  
 660 665 670  
  
 Val Thr Asn Ser Tyr Val Leu Val Pro Leu Asn His Ser Ser Gln Asn  
 675 680 685

<210> 13  
 <211> 687  
 <212> PRT  
 <213> Equus asinus

<400> 13  
 Met Ala Leu Leu Leu Val Ser Leu Leu Ala Phe Leu Ser Leu Gly Ser  
 1 5 10 15

Gly Cys His His Gln Val Cys His Tyr Ser Asn Arg Val Phe Leu Cys  
 20 25 30

Gln Glu Ser Lys Val Thr Glu Ile Pro Ser Asp Leu Pro Arg Asn Ala  
 35 40 45

Leu Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Pro Lys Gly  
 50 55 60

Ala Phe Ser Gly Phe Gly Asp Leu Lys Lys Ile Glu Ile Ser Gln Asn  
 65 70 75 80

Asp Val Leu Glu Val Ile Glu Ala Asn Val Phe Ser Asn Leu Pro Lys  
 85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asp  
 100 105 110

His Asp Ala Phe Gln Asn Leu Pro Asn Leu Gln Tyr Leu Leu Ile Ser

202000-33559652

00000000000000000000000000000000

115	120	125
Asn Thr Gly Ile Lys His Leu Pro Ala Val His Lys Ile Gln Ser Leu		
130	135	140
Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Ile Val		
145	150	155
Glu Arg Asn Ser Phe Met Gly Leu Ser Phe Glu Ser Met Ile Leu Arg		
165	170	175
Leu Ser Lys Asn Gly Ile Gln Glu Ile His Asn Cys Ala Phe Asn Gly		
180	185	190
Thr Gln Leu Asp Glu Leu Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu		
195	200	205
Leu Pro Asn Asp Val Phe Gln Gly Ala Ser Gly Pro Val Ile Leu Asp		
210	215	220
Ile Ser Gly Thr Arg Ile His Ser Leu Pro Asn Tyr Gly Leu Glu Asn		
225	230	235
240		
Leu Lys Lys Leu Arg Ala Arg Ser Thr Tyr Asn Leu Lys Lys Leu Pro		
245	250	255
Ser Leu Glu Lys Phe Val Ala Leu Met Glu Ala Ser Leu Thr Tyr Pro		
260	265	270
Ser His Cys Cys Ala Phe Ala Asn Trp Arg Gln Gln Thr Ser Glu Leu		
275	280	285
Gln Thr Thr Cys Asn Lys Ser Ile Leu Arg Gln Glu Val Asp Met Thr		
290	295	300
Gln Ala Arg Gly Glu Arg Val Ser Leu Ala Glu Asp Asp Glu Ser Met		
305	310	315
320		
Met Tyr Ser Glu Phe Asp Tyr Asp Leu Cys Asn Glu Val Val Asp Val		
325	330	335
Thr Cys Ser Pro Lys Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met		
340	345	350
Gly Tyr Asp Ile Leu Arg Val Leu Ile Trp Phe Ile Ser Ile Leu Ala		
355	360	365
Ile Thr Gly Asn Ile Ile Val Leu Val Ile Leu Ile Thr Ser Gln Tyr		

092601-092659

370	375	380
Lys Leu Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp		
385	390	395
395 400		
Leu Cys Ile Gly Ile Tyr Leu Leu Ile Ala Ser Val Asp Ile His		
405	410	415
415		
Thr Lys Ser Gln Tyr His Asn Tyr Ala Ile Asp Trp Gln Thr Gly Ala		
420	425	430
430		
Gly Cys Asp Ala Ala Gly Phe Phe Thr Val Phe Gly Ser Glu Leu Ser		
435	440	445
445		
Val Tyr Thr Leu Thr Ala Ile Thr Leu Glu Arg Trp His Thr Ile Thr		
450	455	460
460		
His Ala Met Gln Leu Glu Cys Lys Val Gln Leu Arg His Ala Ala Ser		
465	470	475
475 480		
Val Met Leu Val Gly Trp Ile Phe Gly Phe Gly Val Gly Leu Leu Pro		
485	490	495
495		
Ile Phe Gly Ile Ser Thr Tyr Met Lys Val Ser Ile Cys Leu Pro Met		
500	505	510
510		
Asp Ile Asp Ser Pro Leu Ser Gln Leu Tyr Val Met Ser Leu Leu Val		
515	520	525
525		
Leu Asn Val Leu Ala Phe Val Val Ile Cys Gly Cys Tyr Thr His Ile		
530	535	540
540		
Tyr Leu Thr Val Arg Asn Pro Asn Ile Val Ser Ser Ser Ser Asp Thr		
545	550	555
555 560		
Lys Ile Ala Lys Arg Met Gly Ile Leu Ile Phe Thr Asp Phe Leu Cys		
565	570	575
575		
Met Ala Pro Ile Ser Phe Phe Gly Ile Ser Ala Ser Leu Lys Val Ala		
580	585	590
590		
Leu Ile Thr Val Ser Lys Ser Lys Ile Leu Leu Val Leu Phe Tyr Pro		
595	600	605
605		
Ile Asn Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Asn		
610	615	620
620		
Phe Arg Arg Asp Phe Phe Leu Leu Ser Lys Phe Gly Cys Tyr Glu		

625

630

635

640

Met Gln Ala Gln Thr Tyr Arg Thr Glu Thr Ser Ser Thr Gly His Ile  
 645 650 655

Ser His Pro Lys Asn Gly Pro Cys Pro Pro Thr Pro Arg Val Thr Asn  
 660 665 670

Gly Ala Asn Cys Thr Leu Val Pro Leu Ser His Leu Ala Gln Asn  
 675 680 685

&lt;210&gt; 14

&lt;211&gt; 693

&lt;212&gt; PRT

&lt;213&gt; CHICKEN

&lt;400&gt; 14

Met Ser Leu Gly Leu Thr Cys Leu Leu Ile Leu Leu Ala Ser Cys Ser  
 1 5 10 15

Gly Cys Gln His His Thr Cys Leu Cys Glu Gly Arg Ile Phe Ile Cys  
 20 25 30

Gln Glu Ile Lys Val Val Gln Leu Pro Arg Asp Ile Pro Thr Asn Ala  
 35 40 45

Thr Glu Leu Arg Phe Val Leu Thr Lys Met Arg Val Ile Pro Lys Gly  
 50 55 60

Ala Phe Thr Gly Leu His Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn  
 65 70 75 80

Asp Ala Leu Glu Ile Ile Glu Gly Asn Val Phe Ser Ser Leu Pro Lys  
 85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Lys Leu Met Lys Ile Asp  
 100 105 110

Gln Asp Ala Phe Gln His Leu Pro Ser Leu Arg Tyr Leu Leu Ile Ser  
 115 120 125

Asn Thr Gly Leu Ser Phe Leu Pro Val Val His Lys Val His Ser Phe  
 130 135 140

Gln Lys Val Leu Leu Asp Val Gln Asp Asn Ile His Ile Arg Thr Ile  
 145 150 155 160

Glu Arg Asn Thr Phe Met Gly Leu Ser Ser Glu Ser Val Ile Leu Arg  
 165 170 175  
  
 Leu Asn Lys Asn Gly Ile Gln Glu Ile Lys Asp His Ala Phe Asn Gly  
 180 185 190  
  
 Thr Cys Leu Asp Glu Leu Asn Leu Ser Asp Asn Tyr Asn Leu Glu Lys  
 195 200 205  
  
 Leu Pro Glu Lys Val Phe Gln Gly Ala Ile Gly Pro Val Val Leu Asp  
 210 215 220  
  
 Ile Ser Arg Thr Arg Ile Ser Phe Leu Pro Ser His Gly Leu Glu Phe  
 225 230 235 240  
  
 Ile Lys Lys Leu Arg Ala Arg Ser Thr Tyr Lys Leu Lys Lys Leu Pro  
 245 250 255  
  
 Asp Val Asn Lys Phe Arg Ser Leu Ile Glu Ala Asn Phe Thr Tyr Pro  
 260 265 270  
  
 Ser His Cys Cys Ala Phe Thr Asn Arg Lys Thr Gln Asn Thr Glu Phe  
 275 280 285  
  
 Tyr Pro Ile Cys Ser Met Ser Pro Ala Lys Gln Asp Leu Gly Glu Gln  
 290 295 300  
  
 Thr Gly Lys Arg Lys His Arg Arg Ser Ala Ala Glu Asp Tyr Ile Ser  
 305 310 315 320  
  
 His Tyr Gly Thr Arg Phe Gly Pro Val Glu Asn Glu Phe Asp Tyr Gly  
 325 330 335  
  
 Leu Cys Asn Glu Val Val Asp Phe Val Cys Ser Pro Lys Pro Asp Ala  
 340 345 350  
  
 Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Asn Val Leu Arg Val Leu  
 355 360 365  
  
 Ile Trp Phe Ile Asn Ile Leu Ala Ile Thr Gly Asn Thr Thr Val Leu  
 370 375 380  
  
 Ile Ile Leu Ile Ser Ser Gln Tyr Lys Leu Thr Val Pro Arg Phe Leu  
 385 390 395 400  
  
 Met Cys Asn Leu Ala Phe Ala Asp Leu Cys Ile Gly Ile Tyr Leu Leu  
 405 410 415

Phe Ile Ala Ser Val Asp Ile Gln Thr Lys Ser Arg Tyr Tyr Asn Tyr  
 420 425 430  
  
 Ala Ile Asp Trp Gln Thr Gly Ala Gly Cys Asn Ala Ala Gly Phe Phe  
 435 440 445  
  
 Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu Thr Val Ile Thr  
 450 455 460  
  
 Leu Glu Arg Trp His Thr Ile Thr Tyr Ala Met Gln Leu Asn Arg Lys  
 465 470 475 480  
  
 Val Arg Leu Arg His Ala Val Ile Ile Met Val Phe Gly Trp Met Phe  
 485 490 495  
  
 Ala Phe Thr Val Ala Leu Leu Pro Ile Phe Gly Ile Ser Ser Tyr Met  
 500 505 510  
  
 Lys Val Ser Ile Cys Leu Pro Met His Ile Glu Thr Pro Phe Ser Gln  
 515 520 525  
  
 Ala Tyr Val Ile Phe Leu Leu Val Leu Asn Val Leu Ala Phe Val Ile  
 530 535 540  
  
 Ile Cys Ile Cys Tyr Ile Cys Ile Tyr Phe Thr Val Arg Asn Pro Asn  
 545 550 555 560  
  
 Val Ile Ser Ser Asn Ser Asp Thr Lys Ile Ala Lys Arg Met Ala Ile  
 565 570 575  
  
 Leu Ile Phe Thr Asp Phe Leu Cys Met Ala Pro Ile Ser Phe Phe Ala  
 580 585 590  
  
 Ile Ser Ala Ser Leu Arg Val Pro Leu Ile Thr Val Ser Lys Ser Lys  
 595 600 605  
  
 Ile Leu Leu Val Leu Phe Tyr Pro Ile Asn Ser Cys Ala Asn Pro Phe  
 610 615 620  
  
 Leu Tyr Ala Ile Phe Thr Lys Thr Phe Arg Arg Asp Phe Phe Ile Leu  
 625 630 635 640  
  
 Leu Ser Lys Phe Gly Cys Cys Glu Met Gln Ala Gln Ile Tyr Arg Thr  
 645 650 655  
  
 Glu Thr Ser Ser Ser Ala His Asn Phe His Thr Arg Asn Gly His Tyr  
 660 665 670

Pro Thr Ala Ser Lys Asn Ser Asp Gly Thr Ile Tyr Ser Leu Val Pro  
675 680 685

Leu Asn His Leu Asn  
690

<210> 15  
<211> 676  
<212> PRT  
<213> Callithrix jacchus

<400> 15  
Met Lys Gln Pro Leu Leu Ala Leu Gln Leu Leu Lys Leu Leu Leu Leu  
1 5 10 15

Leu Leu Leu Pro Leu Pro Pro Leu Pro Arg Ala Leu Arg Glu Ala Arg  
20 25 30

Cys Cys Pro Glu Pro Cys Asn Cys Thr Pro Asp Gly Ala Leu Arg Cys  
35 40 45

Pro Gly Pro Gly Ala Gly Leu Thr Arg Leu Ser Leu Ala Tyr Leu Pro  
50 55 60

Val Lys Val Ile Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val Ile  
65 70 75 80

Lys Ile Glu Ile Ser Gln Ser Asp Ser Leu Glu Arg Ile Glu Ala Asn  
85 90 95

Ala Phe Asp Asn Leu Leu Asn Leu Ser Glu Ile Leu Ile Gln Asn Thr  
100 105 110

Lys Asn Leu Ile His Ile Glu Pro Gly Ala Phe Thr Asn Leu Pro Arg  
115 120 125

Leu Lys Tyr Leu Ser Ile Cys Asn Thr Gly Ile Arg Lys Phe Pro Asp  
130 135 140

Val Thr Lys Ile Phe Ser Ser Glu Thr Asn Phe Ile Leu Glu Ile Cys  
145 150 155 160

Asp Asn Leu His Ile Thr Thr Ile Pro Gly Asn Ala Phe Gln Gly Met  
165 170 175

Asn Asn Glu Ser Ile Thr Leu Lys Leu Tyr Gly Asn Gly Phe Glu Glu  
180 185 190

Val Gln Ser His Ala Phe Asn Gly Thr Thr Val Ile Ser Leu Val Leu  
195 200 205

Lys Glu Asn Val His Leu Glu Arg Ile His Asn Gly Ala Phe Arg Gly  
210 215 220

Ala Thr Gly Pro Ser Ile Leu Asp Ile Ser Ser Thr Lys Leu Gln Ala  
225 230 235 240

Leu Pro Ser His Gly Leu Glu Ser Ile Gln Thr Leu Ile Ala Thr Ser  
245 250 255

Ser Tyr Ser Leu Lys Lys Leu Pro Ser Arg Glu Lys Phe Ala Asn Leu  
260 265 270

Leu Asp Ala Thr Leu Thr Tyr Pro Ser His Cys Cys Ala Phe Arg Asn  
275 280 285

Val Pro Thr Lys Asp Tyr Pro Ala Ile Phe Ala Glu Ser Gly Gln Ser  
290 295 300

Gly Trp Asp Tyr Asp Tyr Gly Phe His Leu Pro Lys Thr Pro Arg Cys  
305 310 315 320

Ala Pro Glu Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr  
325 330 335

Asp Phe Leu Arg Val Leu Ile Trp Leu Ile Asn Ile Leu Ala Ile Met  
340 345 350

Gly Asn Met Thr Val Leu Phe Val Leu Leu Thr Ser Arg Tyr Lys Leu  
355 360 365

Thr Val Pro Arg Phe Leu Met Cys Asn Leu Ser Phe Ala Asp Phe Cys  
370 375 380

Met Gly Leu Tyr Leu Leu Ile Ala Ser Val Asp Ser Gln Thr Lys  
385 390 395 400

Gly Gln Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Ser Gly Cys  
405 410 415

Asn Thr Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr  
420 425 430

Thr Leu Thr Val Ile Thr Leu Glu Arg Trp His Thr Ile Thr Tyr Ala  
435 440 445

Ile His Leu Asp Gln Lys Leu Arg Leu Arg His Ala Ile Leu Ile Met			
450	455	460	
Leu Gly Gly Trp Leu Phe Ser Ser Leu Ile Ala Met Leu Pro Leu Val			
465	470	475	480
Gly Val Ser Asn Tyr Met Lys Val Ser Ile Cys Leu Pro Met His Ile			
485	490	495	
Glu Thr Pro Phe Ser Gln Ala Tyr Val Ile Phe Leu Leu Val Leu Asn			
500	505	510	
Val Leu Ala Phe Val Ile Ile Cys Ile Cys Tyr Ile Cys Ile Tyr Phe			
515	520	525	
Thr Val Arg Asn Pro Asn Val Ile Ser Ser Asn Ser Asp Thr Lys Ile			
530	535	540	
Ala Lys Lys Met Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys Met Ala			
545	550	555	560
Pro Ile Ser Phe Phe Ala Ile Ser Ala Ala Phe Lys Met Pro Leu Ile			
565	570	575	
Thr Val Thr Asn Ser Lys Val Leu Leu Val Leu Phe Tyr Pro Ile Asn			
580	585	590	
Ser Cys Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Thr Phe Arg			
595	600	605	
Arg Asp Phe Phe Leu Leu Gly Lys Phe Gly Cys Cys Lys His Arg			
610	615	620	
Ala Glu Leu Tyr Arg Arg Lys Asp Phe Ser Ala Tyr Thr Ser Asn Tyr			
625	630	635	640
Lys Asn Gly Phe Thr Gly Ser Ser Lys Pro Ser Gln Ser Thr Leu Lys			
645	650	655	
Leu Pro Ala Leu His Cys Gln Gly Thr Ala Leu Leu Asp Lys Thr Cys			
660	665	670	
Tyr Lys Glu Tyr			
675			

<211> 907  
<212> PRT  
<213> HUMAN

<400> 16  
 Met Asp Thr Ser Arg Leu Gly Val Leu Leu Ser Leu Pro Val Leu Leu  
 1 5 10 15  
  
 Gln Leu Ala Thr Gly Gly Ser Ser Pro Arg Ser Gly Val Leu Leu Arg  
 20 25 30  
  
 Gly Cys Pro Thr His Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu  
 35 40 45  
  
 Arg Val Asp Cys Ser Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu  
 50 55 60  
  
 Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln  
 65 70 75 80  
  
 Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg  
 85 90 95  
  
 Leu Ala Gly Asn Ala Leu Thr Tyr Ile Pro Lys Gly Ala Phe Thr Gly  
 100 105 110  
  
 Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg His  
 115 120 125  
  
 Val Pro Thr Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg  
 130 135 140  
  
 Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly  
 145 150 155 160  
  
 Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu  
 165 170 175  
  
 Ile Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr  
 180 185 190  
  
 Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn  
 195 200 205  
  
 Leu Ser Ser Leu Val Val Leu His Leu His Asn Arg Ile His Ser  
 210 215 220  
  
 Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp

TUD690-35553650

225	230	235	240
Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu			
245	250	255	
Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile			
260	265	270	
Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe			
275	280	285	
Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu			
290	295	300	
Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu			
305	310	315	320
Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr			
325	330	335	
Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro			
340	345	350	
Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro			
355	360	365	
Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn			
370	375	380	
Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu			
385	390	395	400
Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn			
405	410	415	
Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn			
420	425	430	
Leu Leu Ser Ser Phe Pro Ile Thr Gly Leu His Gly Leu Thr His Leu			
435	440	445	
Lys Leu Thr Gly Asn His Ala Leu Gln Ser Leu Ile Ser Ser Glu Asn			
450	455	460	
Phe Pro Glu Leu Lys Val Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys			
465	470	475	480
Ala Phe Gly Val Cys Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn			

109260-935596605

485

490

495

Lys Gly Asp Asn Ser Ser Met Asp Asp Leu His Lys Lys Asp Ala Gly  
 500 505 510

Met Phe Gln Ala Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp  
 515 520 525

Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser  
 530 535 540

Pro Gly Pro Phe Lys Pro Cys Glu His Leu Leu Asp Gly Trp Leu Ile  
 545 550 555 560

Arg Ile Gly Val Trp Thr Ile Ala Val Leu Ala Leu Thr Cys Asn Ala  
 565 570 575

Leu Val Thr Ser Thr Val Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile  
 580 585 590

Lys Leu Leu Ile Gly Val Ile Ala Ala Val Asn Met Leu Thr Gly Val  
 595 600 605

Ser Ser Ala Val Leu Ala Gly Val Asp Ala Phe Thr Phe Gly Ser Phe  
 610 615 620

Ala Arg His Gly Ala Trp Trp Glu Asn Gly Val Gly Cys His Val Ile  
 625 630 635 640

Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr  
 645 650 655

Leu Ala Ala Leu Glu Arg Gly Phe Ser Val Lys Tyr Ser Ala Lys Phe  
 660 665 670

Glu Thr Lys Ala Pro Phe Ser Ser Leu Lys Val Ile Ile Leu Leu Cys  
 675 680 685

Ala Leu Leu Ala Leu Thr Met Ala Ala Val Pro Leu Leu Gly Gly Ser  
 690 695 700

Lys Tyr Gly Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro  
 705 710 715 720

Ser Thr Met Gly Tyr Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys  
 725 730 735

Phe Leu Met Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp

740

745

750

Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Val Lys His Ile  
 755 760 765

Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Asn Cys Pro Val Ala Phe  
 770 775 780

Leu Ser Phe Ser Ser Leu Ile Asn Leu Thr Phe Ile Ser Pro Glu Val  
 785 790 795 800

Ile Lys Phe Ile Leu Leu Val Val Pro Leu Pro Ala Cys Leu Asn  
 805 810 815

Pro Leu Leu Tyr Ile Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val  
 820 825 830

Ser Leu Arg Lys Gln Thr Tyr Val Trp Thr Arg Ser Lys His Pro Ser  
 835 840 845

Leu Met Ser Ile Asn Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser  
 850 855 860

Thr Gln Ala Leu Val Thr Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu  
 865 870 875 880

Pro Pro Ser Ser Val Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys  
 885 890 895

His Leu Ser Ser Val Ala Phe Val Pro Cys Leu  
 900 905

&lt;210&gt; 17

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthesized  
peptide

&lt;400&gt; 17

Arg Ser Phe Ile Lys Ala Glu Asn Thr Thr His Ala Met Ser Ile Lys  
 1 5 10 15

&lt;210&gt; 18

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<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthesized
      peptide

<400> 18
Asp Ile Lys Tyr Arg Gly Gln Tyr Gln Lys Tyr Ala Leu Leu Trp Met
      1           5           10          15
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<210> 19
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthesized
      peptide

<400> 19
Glu Lys Phe Leu Val Ile Val Phe Pro Phe Ser Asn Ile Arg Pro Gly
  1           5           10          15

Lys Arg Gln Thr Ser
  20

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<210> 20
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthesized
      peptide

<400> 20
Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe
      1           5           10          15

Pro Leu Tyr Tyr Asp Gln Thr Glu Asp Ile Gly Ser Lys Gly Tyr Ser

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<210> 21

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized peptide

<400> 21

Ser Ile Gln Lys Thr Ala Leu Gln Thr Thr Glu Val Arg Asn Cys Phe  
1 5 10 15

Gly Arg Glu Val Ala Val Ala Asn Arg

20 25

<210> 22

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized peptide

<400> 22

Arg Val Glu Ile Pro Asp Thr Met Thr Ser Trp  
1 5 10

<210> 23

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized peptide

<400> 23

Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln Leu Leu His Lys His Gln  
1 5 10 15



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<210> 27  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: GAPDH-R1  
reverse primer

<400> 27  
gtgaccaggc gcccaatac 19

<210> 28  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: GAPDH-PVIC  
Taqman(R) Probe

<400> 28  
caaatccgtt gactccgacc ttcacctt 28

<210> 29  
<211> 99  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo 1;  
N=A+G+C+T; K=C+G+T

<400> 29  
cgaagcgtaa gggcccagcc ggccnnknkn nnknnknknkn nnknknknkn knnnknknkn 60  
nnknknknkn nnknknknkn knnkccgggt ccggggccgc 99

<210> 30  
<211> 95  
<212> DNA  
<213> Artificial Sequence

<220>

0995536.002601  
<223> Description of Artificial Sequence: Oligo 2;  
N=A+G+C+T; V=C+A+G

<400> 30  
aaaaggaaaa aagcggccgc vnnvnnvnnv nnvnnvnnvn nvnnvnnvnn vnnvnnvnnv 60  
nnvnnvnnvn nvnnvnnvn gccgccccga cccgg 95

<210> 31  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 31  
Pro Gly Pro Gly Gly  
1 5

<210> 32  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 32  
Asn Val Thr Leu Leu Ser Leu Lys Lys Asn Lys Ile His  
1 5 10

<210> 33  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 33  
Cys Ile Arg His Ile Ser Arg Lys Ala Phe Phe Gly Leu  
1 5 10

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<210> 34
<211> 13
<212> PRT
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<220>
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<400> 34  
His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys  
1 5 10

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<210> 35
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<220>
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<400> 35  
Pro Ile Thr Arg Ile Ser Gln Arg Leu Phe Thr Gly Leu  
1 5 10

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<400> 36  
Glu Lys Thr Phe Ser Ser Leu Lys Asn Leu Gly Glu Leu  
1 5 10

<210> 37  
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<220>  
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polypeptide

<400> 37  
Lys Asn Gln Phe Glu Ser Leu Lys Gln Leu Gln Ser Leu  
1 5 10

<210> 38  
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<220>  
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polypeptide

<400> 38  
Thr Thr His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala  
1 5 10

<210> 39  
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polypeptide

<400> 39  
Ile Glu Asp Ser Ser Ser Leu Lys Leu Gly Val Leu Asn  
1 5 10

<210> 40  
<211> 14  
<212> PRT  
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<400> 40

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Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp  
1 5 10

<210> 41  
<211> 14  
<212> PRT  
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<400> 41  
Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys  
1 5 10

<210> 42  
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<400> 42  
Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu Ser Pro His Leu  
1 5 10

<210> 43  
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polypeptide

<400> 43  
Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn  
1 5 10

<210> 44  
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<212> PRT  
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<400> 44  
Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn  
1 5 10

<210> 45  
<211> 14  
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<220>  
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<400> 45  
Val Leu Asn Lys Ile Thr Leu Gly Asp Ser Ile Met Lys Pro  
1 5 10

<210> 46  
<211> 14  
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<400> 46  
Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile  
1 5 10

<210> 47  
<211> 14  
<212> PRT  
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<400> 47  
Ser Ile Phe Lys Ile Lys Lys Lys Ser Leu Ser Thr Ser Ile  
1 5 10

<210> 48  
<211> 14  
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polypeptide

<400> 48  
Tyr Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala  
1 5 10

<210> 49  
<211> 14  
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<400> 49  
Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu Lys Lys  
1 5 10

<210> 50  
<211> 14  
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<220>  
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polypeptide

<400> 50  
Ile Lys Tyr Leu Thr Asn Ser Thr Phe Leu Ser Cys Asp Ser  
1 5 10

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<210> 51  
<211> 14  
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polypeptide  
  
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Leu Leu Gln Lys Leu Asn Leu Ser Ser Asn Pro Leu Met Tyr  
1 5 10

<210> 52  
<211> 14  
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polypeptide

<400> 52  
Pro Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe Lys Asn  
1 5 10

<210> 53  
<211> 14  
<212> PRT  
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polypeptide

<400> 53  
Phe Ile Lys Ala Glu Asn Thr Thr His Ala Met Ser Ile Lys  
1 5 10

<210> 54  
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<212> PRT  
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093900-05556500  
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<400> 54  
Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn Ala Asn Ser Val Ala  
1 5 10 15

<210> 55  
<211> 16  
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<220>  
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polypeptide

<400> 55  
Phe Gly Thr Val His Gly Asn Ala Asn Ser Val Ala Leu Thr Gln Glu  
1 5 10 15

<210> 56  
<211> 16  
<212> PRT  
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<220>  
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polypeptide

<400> 56  
Asn Lys Asp Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe  
1 5 10 15

<210> 57  
<211> 16  
<212> PRT  
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<220>  
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polypeptide

<400> 57  
Ile Gly Tyr Ser Leu Gly Ile Phe Leu Gly Val Asn Leu Leu Ala Phe  
1 5 10 15

10963536-092601  
<210> 58  
<211> 37  
<212> DNA  
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<223> Description of Artificial Sequence: Synthetic 5'  
primer

<400> 58  
gcagcagcgg ccgcagaata tttgtctggg ttatagc

37

<210> 59  
<211> 36  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic 3'  
primer

<400> 59  
gcagcagtcg acggaaactg gttcattat actgtc

36

<210> 60  
<211> 39  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic 5'  
primer

<400> 60  
gcagcagcgg ccgcattttc ttctacttc atttcatcg

39

<210> 61  
<211> 36  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic 3'

primer

<400> 61  
gcagcagtcg acggttgtga gagtatagag cattgg 36

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